

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Soos, Jeanne M.
Schiffenbauer, Joel
Johnson, Howard M.

(ii) TITLE OF INVENTION: Orally-Administered Interferon-Tau
10 Compositions and Methods

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Dehlinger & Associates
(B) STREET: 350 Cambridge Ave., Suite 250
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
20 (F) ZIP: 94306

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
30 (B) FILING DATE: 15-MAR-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sholtz, Charles K.
35 (B) REGISTRATION NUMBER: 38,615
(C) REFERENCE/DOCKET NUMBER: 5600-0003

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-324-0880
40 (B) TELEFAX: 415-324-0960

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ovis aries

(B) STRAIN: Domestic

(D) DEVELOPMENTAL STAGE: Blastula (blastocyst)

(F) TISSUE TYPE: Trophectoderm

(G) CELL TYPE: Mononuclear trophectoderm cells

(vii) IMMEDIATE SOURCE:

(B) CLONE: oTP-1a

(viii) POSITION IN GENOME:

(C) UNITS: bp

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..516

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Ott, Troy L

Van Heeke, Gino

Johnson, Howard M

Bazer, Fuller W

(B) TITLE: Cloning and Expression in Saccharomyces

cerevisiae of a Synthetic Gene for the Type I

Trophoblast Interferon Ovine Trophoblast

Protein-1:Purification and Antiviral Activity

(C) JOURNAL: J. Interferon Res.

(D) VOLUME: 11

(F) PAGES: 357-364

(G) DATE: 1991

(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	TGC TAC CTG TCG CGA AAA CTG ATG CTG GAC GCT CGA GAA AAT TTA AAA	48
	Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys	
5	1 5 10 15	
	CTG CTG GAC CGT ATG AAT CGA TTG TCT CCG CAC AGC TGC CTG CAA GAC	96
	Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp	
	20 25 30	
10		
	CGG AAA GAC TTC GGT CTG CCG CAG GAA ATG GTT GAA GGT GAC CAA CTG	144
	Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu	
	35 40 45	
15	CAA AAA GAC CAA GCT TTC CCG GTA CTG TAT GAA ATG CTG CAG CAG TCT	192
	Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser	
	50 55 60	
	TTC AAC CTG TTC TAC ACT GAA CAT TCT TCG GCC GCT TGG GAC ACT ACT	240
	Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr	
	65 70 75 80	
	CTT CTA GAA CAA CTG TGC ACT GGT CTG CAA CAG CAA CTG GAC CAT CTG	288
	Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu	
	85 90 95	
25		
	GAC ACT TGC CGT GGC CAG GTT ATG GGT GAA GAA GAC TCT GAA CTG GGT	336
	Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly	
	100 105 110	
30		
	AAC ATG GAT CCG ATC GTT ACT GTT AAA AAA TAT TTC CAG GGT ATC TAC	384
	Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr	
	115 120 125	
35	GAC TAC CTG CAG GAA AAA GGT TAC TCT GAC TGC GCT TGG GAA ATC GTA	432
	Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val	
	130 135 140	
	CGC GTT GAA ATG ATG CGG GCC CTG ACT GTG TCG ACT ACT CTG CAA AAA	480
40	Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys	
	145 150 155 160	
	CGG TTA ACT AAA ATG GGT GGT GAC CTG AAT TCT CCG	516

Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
165 170

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: amino acid sequence of a mature
OvIFNtau protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys
1 5 10 15
Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp
20 25 30
Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu
35 40 45
Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser
50 55 60
Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
65 70 75 80
Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu
85 90 95
Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly
100 105 110
Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr
115 120 125
Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val

130

135

140

Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys
 145 150 155 160

5

Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
 165 170

10 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: synthetic nucleotide sequence encoding
 a mature human interferon-tau protein, HuIFNtau1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

25

TGTGACTTGT CTCAAACCA CGTTTGGTT GGTAGAAAGA ACTTAAGACT ACTAGACGAA 60

ATGAGACGTC TATCTCCACG CTTCTGTCTA CAAGACAGAA AGGACTTCGC TTGCCTCAG 120

30

GAAATGGTTG AAGGTGGCCA ACTACAAGAA GCTCAAGCGA TATCTGTTTT GCACGAAATG 180

TTGCAACAAA GCTTCAACTT GTTCCACACC GAACACTCTT CGGCCGCTTG GGACACCACC 240

TTGTTGGAAC AGCTCAGAAC CGGTTGCAC CAACAATTGG ACAACTTGA TGCATGTTTG 300

35

GGTCAAGTTA TGGGTGAAGA AGACTCTGCT CTCGGGAGAA CCGGTCCAAC GCTAGCTTTG 360

AAGAGATACT TCCAAGGTAT CCACGTTTAC TTGAAGGAAA AGGTTACTC TGACTGTGCT 420

40

TGGGAAACCG TCGTCTAGA AATCATGCGT AGCTTCTCTT CTTTGATCAG CTTGCAAGAA 480

AGATTACGTA TGATGGACGG TGACTTGTCG AGCCCA 516

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: amino acid sequence for a mature
HuIFNtau protein, HuIFNtaul.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg
1 5 10 15
Leu Leu Asp Glu Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp
20 25 30
Arg Lys Asp Phe Ala Leu Pro Gln Glu Met Val Glu Gly Gly Gln Leu
35 40 45
Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser
50 55 60
Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
65 70 75 80
Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu
85 90 95
Asp Ala Cys Leu Gly Gln Val Met Gly Glu Glu Asp Ser Ala Leu Gly
100 105 110
Arg Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile His
115 120 125
Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr Val
130 135 140

Arg Leu Glu Ile Met Arg Ser Phe Ser Ser Leu Ile Ser Leu Gln Glu
 145 150 155 160

Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro
 165 170

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HuIFNtau3, mature no leader sequence

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGT GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC AGC CAG AAC CTC AGG 48
 Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg
 1 5 10 15

CTC CTG GGC CAA ATG AGG AGA CTC TCC CTT CGC TTC TGT CTG CAG GAC 96
 Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp
 20 25 30

AGA AAA GAC TTC GCT TTC CCC CAG GAG ATG GTG GAG GGT GGC CAG CTC 144
 Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu
 35 40 45

CAG GAG GCC CAG GCC ATC TCT GTG CTC CAC GAG ATG CTC CAG CAG AGC 192
 Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser

	50	55	60	
	TTC AAC CTC TTC CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC			240
	Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr			
5	65	70	75	80
	CTC CTG GAG CAG CTC CGC ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG			288
	Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu			
	85	90	95	
10	GAT GCC TGC CTG GGG CAG GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA			336
	Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly			
	100	105	110	
15	AGA ACG GGC CCC ACC CTG GCC ATG AAG AGG TAT TTC CAG GGC ATC CAT			384
	Arg Thr Gly Pro Thr Leu Ala Met Lys Arg Tyr Phe Gln Gly Ile His			
	115	120	125	
20	GTC TAC CTG AAA GAG AAG GGA TAT AGT GAC TGC GCC TGG GAA ATT GTC			432
	Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val			
	130	135	140	
25	AGA CTG GAA ATC ATG AGA TCC TTG TCT TCA TCA ACC AGC TTG CAC AAA			480
	Arg Leu Glu Ile Met Arg Ser Leu Ser Ser Ser Thr Ser Leu His Lys			
	145	150	155	160
30	AGG TTA AGA ATG ATG GAT GGA GAC CTG AGC TCA CCT			516
	Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro			
	165	170		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg

1	5	10	15
Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp			
	20	25	30
5			
Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu			
	35	40	45
Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser			
10	50	55	60
Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr			
	65	70	75
15			
Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu			
	85	90	95
Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly			
	100	105	110
20			
Arg Thr Gly Pro Thr Leu Ala Met Lys Arg Tyr Phe Gln Gly Ile His			
	115	120	125
Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val			
25	130	135	140
Arg Leu Glu Ile Met Arg Ser Leu Ser Ser Ser Thr Ser Leu His Lys			
	145	150	155
30			
Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro			
	165	170	